Microscopic studies on stripe rust-infected doubled haploid wheat lines derived from a cross Kariega × Avocet S

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The wheat cultivar Kariega expresses complete adult plant resistance against yellow rust, causing one of the most important diseases of wheat, whereas Avocet S is susceptible. In former studies, quantitative trait loci analysis of doubled haploid lines derived from a cross Kariega × Avocet S revealed two major-QTL responsible for the adult resistance of Kariega located on chromosome 7D (*Qyr.sgi-7D*) and 2B (*Qyr.sgi-2B.1*) and two minor-QTL located on chromosomes 1A and 4A, whereas Avocet S contains none of these QTL. Stripe rust development was compared in infected flag leaves of the parental lines Kariega and Avocet S to six chosen DH lines, containing all four, none or one QTL by means of fluorescence and confocal laser scanning microscopy. The infection types of the six DH lines ranged from resistant to fully susceptible, depending on the QTL present. No differences in fungal growth were obtained during the first five days post inoculation, whereas the mean size of the fungal colonies started to differ at 6 dpi. Interestingly, DH line MP51 carrying major-QTL 2B responded with lignification to the fungal growth without being able to restrict it, whereas DH line MP35 containing major-QTL 7D did not show lignification, but fungal growth was restricted. First RT PCR experiments resulted in differential expression of known PR proteins, possibly indicating two different pathways or a different timing of these pathways in defence reactions of MP51 and MP35.

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Involvement of nitric oxide during the Russian wheat aphid resistance

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Nitric oxide (NO) is one of the earliest molecules produced during the hypersensitive response in plants. The current study was conducted to investigate the involvement of NO during the resistance responses of wheat (*Triticum aestivum* L.) to the Russian wheat aphid (RWA), *Diuraphis noxia*. The resistant (cv. *Tugela DN*) and near-isogenic susceptible (*Tugela*) wheat plants were used for this purpose. RWA infestation selectively induced early production of NO to higher level in resistant than susceptible plants. Further experiments were conducted and the obtained results suggested nitrate reductase to be the key enzyme responsible for this NO production. Results on the *in vitro* and *in vivo* studies suggest that NO could be a signal molecule of the downstream defence responses during the resistance responses of wheat against the RWA. Further research to elucidate the role played by nitric oxide in RWA–wheat interaction is still conducted.

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A taxonomic revision of the genus *Millettia* in South Africa

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The widely distributed genus *Millettia*, is represented in South Africa by only two species, namely *M. grandis* and *M. stuhlmannii*. The third species recorded from South Africa as *M. sutherlandii* belongs to the genus *Lonchocarpus*. The two species both belong to section Compresso-Gemmatae. A revision of the genus in South Africa is presented. Typification, complete synonymy and correct nomenclature for the species, as well as geographical distribution are also given. The ethnobotany and chemistry of the two species are also explored.

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Effects of climate warming on typical southern African Proteaceae: A demographic perspective

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Climate warming scenarios project greater increases in daily temperature minima than maxima, these and the consequent reductions in diurnal temperature amplitudes expected to have negative consequences for post-fire seedling recruitment in Proteaceae. This hypothesis was tested by examining seedling recruitment and growth responses of 8 typical species to soil temperatures artificially elevated 4 °C and 6 24 °C above ambient with overhead infrared lamps in outdoor microcosms. The measured

recruitment responses were incorporated into a simple stochastic demographic model to predict likelihoods of localized extinction of natural species populations from their current densities listed as 0.2 km^2 point locality records in a Protea Atlas Database. Seven of the eight Proteaceae species tested exhibited diminished seedling recruitment, both in absolute amounts (total germination) and rate (germination vigour), under the experimentally enhanced soil temperatures. However, seedling masses were increased, an outcome of less intense intra-specific competition between individual seedlings resulting from smaller population densities linked to the diminished seedling recruitment with experimental warming. The demographic model predicted comparatively less severe climate warming impacts on Proteaceae species distributions and a different perspective on these than those projected by bioclimatic models encompassing the entire plant life cycle. It forecast the disappearance over 5 fire cycles spanning an approximate 50 to 100 year period of predominantly low density populations currently occurring in relatively consistent though mostly small fractions ($\geq$17% of total populations) throughout species distributions ranges. The consequences of which would be increased fragmentation of already disjointed Proteaceae species populations with only minor ($\geq$5%) contraction in their overall distribution ranges. It is concluded that the demographic model applied could supplement the bioclimatic model approach by providing an empirically based means of identifying which Proteaceae species populations at precisely specified locations are at greatest risk of disappearing with climate warming so appropriate mitigation measures can be considered.

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From jelly beans to jumping genes — Application of biotechnology in conifers

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Conifer biotechnology has been implemented in many of the most commercially important forest tree species worldwide using techniques such as *in vitro* clonal propagation, microarray technology, synthetic seed technology through to genetic modification. South Africa is classified as a water-scarce country due to an average annual rainfall of approximately 450 mm/annum. Intensive forestry requires 800 mm/annum or more. This has directed the attention of the South African forestry industry towards quality product-based selection rather than exploitation of natural resources and indigenous forests. The integration of biotechnology has the potential for molecular tree improvement; as well as assisting in plantation site constraints, and in making mill processes more efficient and environmentally-friendly. This paper will serve to review recent advances in forest biotechnology, which have culminated in progress relevant to the South African forestry industry.

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Molecular phylogeny supports model of bulb evolution in southern African *Oxalis*: Morphological and taxonomic implications

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Oxalis is virtually unique amongst the non-monocot angiosperms in exhibiting a true bulbous growth form; both southern African and South American members of the genus display this trait. Bulbs of the southern African taxa differ from their South American counterparts in that their leaf bases have lost petiolar and laminar extensions, and their above-ground plant organs are borne on a seasonal rhizome. Recent morphological and anatomical studies focusing on the bulbs of the southern African taxa have clarified the identities of many underground structures, and have allowed a model of bulb evolution to be proposed. This model allows for the typical angiosperm stem and leaf architecture of oxalidaceous relatives to be successively transformed into the bulb structures present in South American and southern African species. It successfully explains the major differences between these bulb types and utilizes a diversity of extant underground structures as putative intermediates. Moreover, patterns of relationships evident in recent DNA-based phylogenetic reconstructions of the genus *Oxalis* are highly congruent with the steps implied by the model. These patterns support a single origin for the bulbous growth form in the genus, and a close relationship between the South American and southern African taxa. The proposed model has important implications for the tremendous morphological diversity present in the southern African species, where the above-ground architecture between closely-related (and even within) species can be radically different. Numerous species have an above-ground stem–leaf arrangement analogous to that of the bulb, and several taxa bear bulbils in the axils of the leaves. These characters are considered evidence for the co-opting of the typical bulb architecture onto above-ground structures. Such a mechanism would also explain the